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- -> UCSC Query

Genotyping

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Annotation Views

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Full Record

Details for HUGENEFL:M64347_AT

Full Screen

Cluster Members NetAffx Links

Consensus/Exemplar

GeneChip Array Information

Probe Set ID M64347_at

GeneChip HumanGeneFL Array Array

Organism Common Human

Name

Probe Design Information

Transcript ID M64347

Sequence Exemplar sequence Type

Representative M64347 NCBI

Public ID

M64347, class A, 20 probes, 20 in M64347 3336-3720, Human novel growth facto Target Description receptor mRNA, 3' cds

Genomic Alignment of Target Sequence

April 2003 (NCBI 33) Assembly

% Identity Cytoband **Position** Alignment(s) 93 p16.3 chr4: 1771773-1772182 (+) UCSC

Representative **UniGene Description Position** Transcript fibroblast growth factor receptor 3 NM 000142 chr4:1757261-(achondroplasia, thanatophoric 1772237 (+) UCSC Overlapping **NCBI** dwarfism) **Transcripts** fibroblast growth factor receptor 3 chr4:1757261-NM 022965 (achondroplasia, thanatophoric 1772237 (+) UCSC **NCBI** dwarfism)

Public Domain and Genome References

fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) Gene Title

Gene Symbol FGFR3 HGNC

Chromosomal Location

4p16.3

Hs.1420 NCBI (FULL LENGTH) UniGene ID ENSG00000068078 Ensembl

Ensembl

2261 NCBI LocusLink

P22607 EMBL-EBI

 SwissProt
 Q96T34 EMBL-EBI Q96T35 EMBL-EBI Q96T36 EMBL-EBI Q9NRB6 EMBL-EBI 2.7.1.112

OMIM 134934 NCBI
RefSeq Protein NP_000133 NCBI

RefSeq Protein NP_000133 NCBI ID NP_075254 NCBI

RefSeq Transcript ID RefSeq Title

RefSeq NM_000142 NCBI fibroblast growth factor receptor 3 isoform 1 precursor NM_022965 NCBI fibroblast growth factor receptor 3 isoform 2 precursor

Functional Annotations

	1 unetioniii	I KINI O WATER		
	ID	Title	Organism	Type
	DROSGENOME1:143549_AT	breathless	Drosophila	Putative Ortholog
	RAE230A:1369373_AT	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	RAE230B:1384056_AT	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	RAE230B:1384829_AT	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	RG-U34B:RC_AA899336_AT	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	RG-U34C:RC_Al136304_AT	fibroblast growth factor receptor 3	Rat	Putative Ortholog
Ortholog	RG-U34C:RC Al145424 AT fibroblast growth factor Rat receptor 3		Rat	Putative Ortholog
	MG-U74AV2:160919_R_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MG-U74AV2:162253 AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MOE430A:1421841_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MOE430A:1425796_A_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MU11KSUBA:M81342 S_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
,	MOUSE430_2:1421841_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MOUSE430 2:1425796 A AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MOUSE430A 2:1421841_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MOUSE430A_2:1425796_A_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	GO Biological Process (view grap	oh)		

GO Biological Process (view graph)

ID	Description	Evidence	Links
165	MAPKKK cascade	experimental evidence	QuickGO AmiGO
1501	skeletal development	predicted/computed	QuickGO AmiGO
7048	oncogenesis	experimental evidence	QuickGO AmiGO
7259	JAK-STAT cascade	experimental	QuickGO

						evidence		<u>AmiGC</u>	<u>)</u>
	8543 FG	F rec	eptor sign	aling	pathway	experime evidence		Quick@ AmiGC	
	GO Cellu	ılar Co	mponent	(view	graph)				
	ID		Descr	iption	1		idence		inks
Gene Ontology	5887 into	egral 1	to plasma	mem	brane	experime evidence	experimental <u>QuickGO</u> evidence <u>AmiGO</u>		
	GO Mole	cular	Function (view	graph)				
	ID		Descr	iption	1	Ev	idence		inks
		roblas tivity	t growth fa	actor	receptor	experime evidence		Quick@ AmiGC	
	Meth	od	ID			Descripti	on	E	-Value
	blast		1311204	8	fibroblast gro isoform 2 pro protein kinas [Homo sapie	ecursor; h se; tyrosin		0.0 4	
Protein Similarities	blast		1318625	5	fibroblast gro isoform 3 pro growth facto protein; prot receptor like bacteria-exp growth facto tyrosylprotei protein kinas	ecursor; k r receptor ein tyrosir 14; FGF ressed kir r receptor n kinase;	eratinocyte ; K-sam ne kinase, receptor; nase; fibroblas BEK; hydroxyaryl-	0.0 st	
	blast		4503711		fibroblast gro isoform 1 pro protein kinas [Homo sapie	ecursor; h se; tyrosin		0.0 4	
	blast		20452380	0				0.0	
	Method		ID			Descript	ion		E-Value
	Hanks	FGF	<u>R-3</u>	PTK tyro	(Group B me	embrane s PTK XV F	KINASES:5.6 panning prote Fibroblast grov FR-3	ein	1.0E- 166
Protein Families	ec	<u>ZA70</u>	AAMUH (PRO KDA	OTEIN KINAS	SE ZAP-70 OCIATED	12:TYROSINI) (EC 2.7.1.11 PROTEIN) (\$ IASE).	12) (70	7.38E- 99
	Hanks	FGF	R-3	PTK tyro	(Group B me	embrane s PTK XV F	KINASES:5.6 panning prote Tibroblast grov FR-3	ein	1.0E- 167
	ec	<u>ZA70</u>	AAMUH_C	PRO KDA	OTEIN KINAS	SE ZAP-70 OCIATED	12:TYROSINI) (EC 2.7.1.11 PROTEIN) (\$ IASE).	12) (70	7.38E- 99
	Databas	e	ID			Description	on		E-Value
	scop	<u>d1</u>			oa_SCOP:d. r receptor 2	144.1.2:	Fibroblast gro	wth	3.81E- 81
	scop	<u>d1</u>			2e1 SCOP:b		oroblast grow	th	4.95E- 21
	scop	<u>d1</u>	gjoa_		oa_ SCOP:d. or receptor 2	144.1.2:	Fibroblast gro	wth	3.81E- 81

	scop	<u>d1ev2e1</u>	d1ev2e1 SCOP:b.1.1.4: Fibroblast growth factor receptor, FGFR	4.25E- 21
	pfam	<u>ig</u>	Immunoglobulin domain	1.6E-5
	pfam	ig	Immunoglobulin domain	3.2E-8
	pfam	<u>pkinase</u>	Protein kinase domain	2.3E-92
	pfam	<u>ig</u>	Immunoglobulin domain	1.6E-5
	pfam	<u>ig</u>	Immunoglobulin domain	3.2E-8
	pfam	<u>pkinase</u>	Protein kinase domain	2.3E-92
	pfam	<u>ig</u>	Immunoglobulin domain	7.3E-8
	InterPro	IPR000719 EMBL-EBI	Protein kinase	
Protein Domains	InterPro	IPR007110 EMBL-EBI	Immunoglobulin-like	
	InterPro	IPR001245 EMBL-EBI	Tyrosine protein kinase	
	InterPro	IPR008266 EMBL-EBI	Tyrosine protein kinase, active site	
	InterPro	IPR003598 EMBL-EBI	Immunoglobulin C-2 type	

Trans Membrane

ID	Number Of Domains	Probability of Interior N-Terminus
NP_000133	2	0.11005

Sequence

Target Sequence >HUGENEFL:M64347_AT ${\tt gacttcaaagcaagctggtatttcatacaaattcttctaattgctgtgtcccaggca}$ $\tt gggagacggtttccagggaggggccggccctgtgtgcaggttccgatgttattagatgtt$ agacttaacacttcttacgcaatgcttctagagttttatagcctggactgctacctttca ${\tt aagcttggagggaagccgtgaattcagttggttcgttctgtactgttactgggccctgag}$ tctgggcagctgtcccttgcttgcctgcagggccatggctcagggtggtctcttcttggg gcccagtgcatggtggccagaggtgtcacccaaaccggcaggtgcgatt

	Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
	GACTTCAAAGCAAGCTGGTATTTTC	359	161	3348	Antisense
	CATACAAATTCTTCTAATTGCTGTG	360	161	3372	Antisense
	AATTCTTCTAATTGCTGTGTGTCCC	361	161	3378	Antisense
	TGCTGTGTCCCAGGCAGGGAGAC	362	161	3390	Antisense
	TGTGTGCAGGTTCCGATGTTATTAG	363	161	3438	Antisense
	TCTTACGCAATGCTTCTAGAGTTTT	364	161	3540	Antisense
	GCAATGCTTCTAGAGTTTTATAGCC	365	161	3546	Antisense
Probe Info	GAGTTTTATAGCCTGGACTGCTACC	366	161	3558	Antisense
	TGCTACCTTTCAAAGCTTGGAGGGA	367	161	3576	Antisense
	AAGCTTGGAGGGAAGCCGTGAATTC	368	161	3588	Antisense
	TGAATTCAGTTGGTTCGTTCTGTAC	369	161	3606	Antisense
	GTTCGTTCTGTACTGTTACTGGGCC	370	161	3618	Antisense
	CTGGGCCCTGAGTCTGGGCAGCTGT	371	161	3636	Antisense
	CCTGAGTCTGGGCAGCTGTCCCTTG	372	161	3642	Antisense
	TCTGGGCAGCTGTCCCTTGCTTGCC	373	161	3648	Antisense
	TCCCTTGCTTGCCTGCAGGGCCATG	374	161	3660	Antisense

GCTTGCCTGCAGGGCCATGGCTCAG	375	161	3666	Antisense
CTTGGGGCCCAGTGCATGGTGGCCA	376	161	3702	Antisense
GTGGCCAGAGGTGTCACCCAAACCG	377	161	3720	Antisense
GTCACCCAAACCGGCAGGTGCGATT	378	161	3732	Antisense

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